



MP

RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/048,146A
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Date Processed by STIC: 6/4/2002

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FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

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PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/048,146A

DATE: 06/04/2002

TIME: 16:18:15

Input Set : A:\62068.app

Output Set: N:\CRF3\06042002\J048146A.raw

see p. 5
Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Tsang et al.
5 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING LARVAL TAENIA SOLIUM
7 <130> FILE REFERENCE: 6395-62068
9 <140> CURRENT APPLICATION NUMBER: 10/048,146A
10 <141> CURRENT FILING DATE: 2002-04-18
12 <150> PRIOR APPLICATION NUMBER: US 60/147,318
13 <151> PRIOR FILING DATE: 1999-08-03
15 <150> PRIOR APPLICATION NUMBER: PCT/US00/21173
16 <151> PRIOR FILING DATE: 2000-08-03
18 <160> NUMBER OF SEQ ID NOS: 9
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 2153
24 <212> TYPE: DNA
25 <213> ORGANISM: Taenia solium
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (145)..(531)
30 <223> OTHER INFORMATION:
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36 agggaaagca tacgataaac ataaaccaat gctggttata taagagacga tctcggctac 120
38 acttgtaact gaacaacctg taga atg cgt gcc tac att gtg ctt ctc gct 171
39 Met Arg Ala Tyr Ile Val Leu Leu Ala
40 1 5
42 ctc act gtt ttc gta gtg acg gtg tcg gcc gag tgg gtg ccc att tcg 219
43 Leu Thr Val Phe Val Val Thr Val Ser Ala Glu Trp Val Pro Ile Ser
44 10 15 20 25
46 agt gtc cac ata gcc tca tgc aaa agc cac tac atg ttc caa tta aaa 267
47 Ser Val His Ile Ala Ser Cys Lys Ser His Tyr Met Phe Gln Leu Lys
48 30 35 40
50 cgc ttt ttt gcc ttt agg aaa aac aaa ccg aaa gat gtt gca aat agt 315
51 Arg Phe Phe Ala Phe Arg Lys Asn Lys Pro Lys Asp Val Ala Asn Ser
52 45 50 55
54 acg aaa aaa ggg ata gaa tat gtc cac gaa ttc ttc cac gaa gac ccg 363
55 Thr Lys Lys Gly Ile Glu Tyr Val His Glu Phe Phe His Glu Asp Pro
56 60 65 70
58 att ggt aaa caa att gct caa ctc gca aag gaa tgg aag gaa gca atg 411
59 Ile Gly Lys Gln Ile Ala Gln Leu Ala Lys Glu Trp Lys Glu Ala Met
60 75 80 85
62 ttg gaa ggt agg ttt tgg tgt ttt ctg tca gaa gaa aat tat cta ttc 459
63 Leu Glu Gly Arg Phe Trp Cys Phe Leu Ser Glu Glu Asn Tyr Leu Phe
64 90 95 100 105

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66 att cat cta gac aaa ggc aaa ata cgg acg tca ctg gtt gag cac tgc      507
67 ile his leu asp lys gly lys ile arg thr ser leu val glu his cys
68              110              115              120
70 aaa ggt cct aag aaa aaa act gct taacttgatgca actttcatgca gttcttctct      561
71 lys gly pro lys lys lys thr ala
72              125
74 tcactaataa atgctcatta ataagaaagc tgccttttgc aagatcaacg agggccatag      621
76 actgtgaggg ttatagccta aggttatggg gtgaaatgag ataggaattg agcatttgag      681
78 aagttactaa tttaaattga aagccgcatt tcttctgcaa ttgacgtgtg atggtttagcg      741
80 aaaccaagtg aagcacgacc tcttgagtcg tttcaacagc cgccagtggg ttaccacagt      801
82 gcttcaccag tgggtagact ggtttgtcac acatgcgagg tacggtcaga gggctaacag      861
84 gtgtggtgga ggggccaaca cgtgtaagac aagcagttcc ctttctctgt cgtgaggcac      921
86 actcagcacc cacctcgttt acttctccct tgacgactgt aatgcatttg gggtcaccat      981
88 gccccgccca agttgaaggc actgatgaca tttgtaccat atcaccgata agtattaact     1041
90 ctccacttc ccagattttg aggtcaggcg atcctactga ctcggtgtag ccccatgggt      1101
92 gtccatgctc tgcaccattc gctgttcagt ggagcatcca cctagacggc caaccaatct      1161
94 cgcctccctt ctctgtgtct caagatgtgc gtcggtgaga tttggagggt ctgatcacca      1221
96 tactaaccac gtaggtttca tcatctctaa gaagcaccac ttcttgaggt cgcattgtgt      1281
98 accaccagcc ggtgtaatca agagtgaact tcgcgtcacc cctaagaagg ctatagatct      1341
100 gcaagtcagc gcaatagctt cagccatgct gactaaaatg tgtaaggagc cagtagctct      1401
102 agcccaacac aagtggagct aataatgggc ttcccagat acatgaatcc caaatcggtg      1461
104 agcatggggc atgaatatgg cttcttgagt cttccttgaa tgcaaacgaa ggcatagcac      1521
106 gagggtagga tgagtgtaca gaaaacagcg aggcaacgaa tctactggca tggccctgat      1581
108 gccacccgc ccagctaggg tagtttgcc acctcagtc ttaatcgaat gcgagcagca      1641
110 gaacaaacaa agtattacat agccacactc ttcttttgag cgtcgtcctc gacgctcctt      1701
112 tcgacacacc tcccgcatca gccaccacaa agtaatcagt actggggaga caccacagag      1761
114 ctaaccgtgc cagtcatgga aaatttgacg gcaactgagg agatgcctga ccccttttg      1821
116 cagttcgaat gctgcccgtg gtcaaactcc tgcacagcc atcacctacg attcaaact      1881
118 cctagtcgcc aaattttcgt gaacctcta aaattttcgt gcactctcaa gacacttcca      1941
120 actgacttag agctttttca tttggtgaga acacgtaaaa gcttcaagta aacaacaggc      2001
122 aacgatttca ctttgatgct ctaccatca attctcttgt atgtgccacc acctaaacc      2061
124 ctccctgacc acttccactc tctctctctc cctaaataac aacacttgga agcatgaatg      2121
126 gtgtctgtca aagttacacc cctagactgc ag                                2153
129 <210> SEQ ID NO: 2
130 <211> LENGTH: 129
131 <212> TYPE: PRT
132 <213> ORGANISM: Taenia solium
134 <400> SEQUENCE: 2
136 Met Arg Ala Tyr Ile Val Leu Leu Ala Leu Thr Val Phe Val Val Thr
137 1              5              10              15
140 Val Ser Ala Glu Trp Val Pro Ile Ser Ser Val His Ile Ala Ser Cys
141              20              25              30
144 Lys Ser His Tyr Met Phe Gln Leu Lys Arg Phe Phe Ala Phe Arg Lys
145              35              40              45
148 Asn Lys Pro Lys Asp Val Ala Asn Ser Thr Lys Lys Gly Ile Glu Tyr
149              50              55              60
152 Val His Glu Phe Phe His Glu Asp Pro Ile Gly Lys Gln Ile Ala Gln
153 65              70              75              80
156 Leu Ala Lys Glu Trp Lys Glu Ala Met Leu Glu Gly Arg Phe Trp Cys

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157          85          90          95
160 Phe Leu Ser Glu Glu Asn Tyr Leu Phe Ile His Leu Asp Lys Gly Lys
161          100          105          110
164 Ile Arg Thr Ser Leu Val Glu His Cys Lys Gly Pro Lys Lys Lys Thr
165          115          120          125
168 Ala
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173 <211> LENGTH: 298
174 <212> TYPE: DNA
175 <213> ORGANISM: Taenia solium
177 <220> FEATURE:
178 <221> NAME/KEY: CDS
179 <222> LOCATION: (3)..(224)
180 <223> OTHER INFORMATION:
183 <400> SEQUENCE: 3
184 ta ttc gta gtg gcg gtt tcg gcc gag aaa aac aaa ccg aag tgt gat      47
185   Phe Val Val Ala Val Ser Ala Glu Lys Asn Lys Pro Lys Cys Asp
186   1          5          10          15
188 gca aat agt act aag aaa gag ata gaa tat atc cac aat tgg ttt ttc      95
189 Ala Asn Ser Thr Lys Lys Glu Ile Glu Tyr Ile His Asn Trp Phe Phe
190          20          25          30
192 cat gat gac ccg att gga aaa caa att gct caa ctc gca aag gac tgg      143
193 His Asp Asp Pro Ile Gly Lys Gln Ile Ala Gln Leu Ala Lys Asp Trp
194          35          40          45
196 aat gaa aca gtg cag gaa gcc aaa ggc aaa ttt tgg gcg tca ctg gct      191
197 Asn Glu Thr Val Gln Glu Ala Lys Gly Lys Phe Trp Ala Ser Leu Ala
198          50          55          60
200 gag tac tgc aga ggt ctg aag aac aaa act gct taacttgtca actttcatgc      244
201 Glu Tyr Cys Arg Gly Leu Lys Asn Lys Thr Ala
202          65          70
204 gttcttctct tcaccaataa atgctgatta acaagaaaaa aaaaaaaaaa aaaa      298
207 <210> SEQ ID NO: 4
208 <211> LENGTH: 74
209 <212> TYPE: PRT
210 <213> ORGANISM: Taenia solium
212 <400> SEQUENCE: 4
214 Phe Val Val Ala Val Ser Ala Glu Lys Asn Lys Pro Lys Cys Asp Ala
215 1          5          10          15
218 Asn Ser Thr Lys Lys Glu Ile Glu Tyr Ile His Asn Trp Phe Phe His
219          20          25          30
222 Asp Asp Pro Ile Gly Lys Gln Ile Ala Gln Leu Ala Lys Asp Trp Asn
223          35          40          45
226 Glu Thr Val Gln Glu Ala Lys Gly Lys Phe Trp Ala Ser Leu Ala Glu
227          50          55          60
230 Tyr Cys Arg Gly Leu Lys Asn Lys Thr Ala
231 65          70
234 <210> SEQ ID NO: 5
235 <211> LENGTH: 294
236 <212> TYPE: DNA

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237 <213> ORGANISM: Taenia solium
239 <220> FEATURE:
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241 <222> LOCATION: (3)..(221)
242 <223> OTHER INFORMATION:
245 <400> SEQUENCE: 5
246 tt ttc gta gtg gcg gtg tcg gcc gag gaa act aaa cca gag gac gtg      47
247   Phe Val Val Ala Val Ser Ala Glu Glu Thr Lys Pro Glu Asp Val
248   1          5          10          15
250 gta aag aat att aag aaa ggg atg gaa gtt gtc tac aaa ttt ttc tac      95
251 Val Lys Asn Ile Lys Lys Gly Met Glu Val Val Tyr Lys Phe Phe Tyr
252          20          25          30
254 gaa gac ccg ttg gga aag aaa ata gct caa ctc gca aag gac tgg aag      143
255 Glu Asp Pro Leu Gly Lys Lys Ile Ala Gln Leu Ala Lys Asp Trp Lys
256          35          40          45
258 gaa gca atg ttg gaa gcc aga agc aaa gtg cgg gcg tca ctg gct gag      191
259 Glu Ala Met Leu Glu Ala Arg Ser Lys Val Arg Ala Ser Leu Ala Glu
260          50          55          60
262 tac atc aga ggt ctc aag aac gaa gct gct taacttgta actttcatgc      241
263 Tyr Ile Arg Gly Leu Lys Asn Glu Ala Ala
264          65          70
266 gttcttctct tcactaataa atgctcatta ataagaaaaa aaaaaaaaaa aaa      294
269 <210> SEQ ID NO: 6
270 <211> LENGTH: 73
271 <212> TYPE: PRT
272 <213> ORGANISM: Taenia solium
274 <400> SEQUENCE: 6
276 Phe Val Val Ala Val Ser Ala Glu Glu Thr Lys Pro Glu Asp Val Val
277 1          5          10          15
280 Lys Asn Ile Lys Lys Gly Met Glu Val Val Tyr Lys Phe Phe Tyr Glu
281          20          25          30
284 Asp Pro Leu Gly Lys Lys Ile Ala Gln Leu Ala Lys Asp Trp Lys Glu
285          35          40          45
288 Ala Met Leu Glu Ala Arg Ser Lys Val Arg Ala Ser Leu Ala Glu Tyr
289          50          55          60
292 Ile Arg Gly Leu Lys Asn Glu Ala Ala
293 65          70
296 <210> SEQ ID NO: 7
297 <211> LENGTH: 6
298 <212> TYPE: PRT
299 <213> ORGANISM: Taenia solium
301 <400> SEQUENCE: 7
303 Ile Ala Gln Leu Ala Lys
304 1          5
307 <210> SEQ ID NO: 8
308 <211> LENGTH: 24
309 <212> TYPE: PRT
310 <213> ORGANISM: Taenia solium
312 <220> FEATURE:

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313 <221> NAME/KEY: variant *Asp can only represent itself, nothing else. Use Xaa*
 314 <222> LOCATION: (7)..(8)
 315 <223> OTHER INFORMATION: Amino acid at position 7 may also be valine *and*
 318 <220> FEATURE:
 319 <221> NAME/KEY: site *explain variation*
 320 <222> LOCATION: (21)..(22)
 321 <223> OTHER INFORMATION: Asparagine at position 21 is an amino acid insertion *in the*
 324 <220> FEATURE:
 325 <221> NAME/KEY: variant *use Xaa and explain*
 326 <222> LOCATION: (14)..(15)
 327 <223> OTHER INFORMATION: Amino acid at position 14 may also be glycine *<225>-<223> section.*
 330 <220> FEATURE:
 331 <221> NAME/KEY: variant *use Xaa*
 332 <222> LOCATION: (18)..(19)
 333 <223> OTHER INFORMATION: Amino acid at position 18 may also be valine
 336 <220> FEATURE:
 337 <221> NAME/KEY: variant *use Xaa*
 338 <222> LOCATION: (19)..(20)
 339 <223> OTHER INFORMATION: Amino acid at position 19 may also be histidine
 342 <220> FEATURE:
 343 <221> NAME/KEY: variant *use Xaa*
 344 <222> LOCATION: (20)..(21)
 345 <223> OTHER INFORMATION: Amino acid at position 20 may also be arginine
 348 <400> SEQUENCE: 8
 350 Lys Asn Lys Pro Lys Asp (Asp) Ala Ala Ser Thr Lys Lys (Glu) Ile Glu
 351 1 5 10 15
 354 Tyr (Ile) (Trp) (His) Asn Phe Phe Phe
 355 20
 358 <210> SEQ ID NO: 9
 359 <211> LENGTH: 13
 360 <212> TYPE: PRT
 361 <213> ORGANISM: Taenia solium *same errors as above*
 363 <220> FEATURE:
 364 <221> NAME/KEY: variant
 365 <222> LOCATION: (5)..(6)
 366 <223> OTHER INFORMATION: Amino acid at position 5 may also be isoleucine
 369 <220> FEATURE:
 370 <221> NAME/KEY: variant
 371 <222> LOCATION: (12)..(13)
 372 <223> OTHER INFORMATION: Amino acid at position 12 may also be aspartic acid
 375 <220> FEATURE:
 376 <221> NAME/KEY: variant
 377 <222> LOCATION: (7)..(9)
 378 <223> OTHER INFORMATION: Amino acid at position 7 may also be asparagine
 381 <220> FEATURE:
 382 <221> NAME/KEY: site
 383 <222> LOCATION: (8)..(9)
 384 <223> OTHER INFORMATION: Tryptophan at position 8 is an amino acid insertion
 387 <400> SEQUENCE: 9

VERIFICATION SUMMARY

DATE: 06/04/2002

PATENT APPLICATION: US/10/048,146A

TIME: 16:18:16

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date